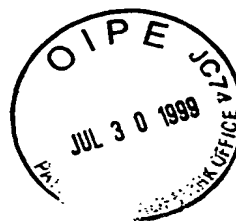


# SEQUENCE LISTING



<110> WATANABE, Eijiro  
OEDA, Kenji

<120> Raffinose Synthase Genes and Their Use

<130> 0020-4348P

<140> 08/992,914

<141> 1997-12-18

<150> 8-338673/1996 JAPAN

<151> 1996-12-18

<160> 86

<170> PatentIn Ver. 2.0

<210> 1

<211> 2746

<212> DNA

<213> Vicia faba

<220>

<221> CDS

<222> (101)..(2497)

<400> 1

aattttcaag catagccaag ttaaccacct tagaaacatt cctacaagct acttatccct 60

gtcaataagc tactaagcta ccagagtctc atcaatcacc atg gca cca cca agc 115  
Met Ala Pro Pro Ser  
1 5

ata acc aaa act gca acc ctc caa gac gta ata agc acc atc gat att 163  
Ile Thr Lys Thr Ala Thr Leu Gln Asp Val Ile Ser Thr Ile Asp Ile  
10 15 20

ggt aat ggt aac tca ccc tta ttc tcc ata acc tta gac caa tca cgt 211  
Gly Asn Gly Asn Ser Pro Leu Phe Ser Ile Thr Leu Asp Gln Ser Arg  
25 30 35

gac ttc ctt gca aat ggc cac cct ttc ctc acc caa gtc cca cct aac 259  
Asp Phe Leu Ala Asn Gly His Pro Phe Leu Thr Gln Val Pro Pro Asn  
40 45 50

ata aca aca aca aca aca acc act gct tcc tct ttt ctc aat ctc aaa 307  
Ile Thr Thr Thr Thr Thr Thr Thr Ala Ser Ser Phe Leu Asn Leu Lys  
55 60 65

tcc aac aaa gat acc att ccc aac aac aac aac acc atg ttg ttg caa 355  
Ser Asn Lys Asp Thr Ile Pro Asn Asn Asn Asn Thr Met Leu Leu Gln  
70 75 80 85

caa ggt tgt ttc gtt ggt ttc aac tcc acc gaa ccc aaa agc cac cac 403  
Gln Gly Cys Phe Val Gly Phe Asn Ser Thr Glu Pro Lys Ser His His  
90 95 100

gta gtt cca ctc ggc aaa cta aaa gga atc aaa ttc atg agc ata ttc 451  
Val Val Pro Leu Gly Lys Leu Lys Gly Ile Lys Phe Met Ser Ile Phe

105										110					115																											
cg	g	t	t	a	a	a	g	t	t	t	g	g	a	c	a	a	c	t	t	c	a	c	t	g	g	t	g	c	g	a	a	c	a	a	t	g	g	a	c	a	g	499
Arg	Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Thr	Asn	Gly	Gln																											
		120						125				130																														
g	a	a	c	a	a	c	a	a	a	t	a	a	t	a	a	c	a	a	t	a	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	547			
Glu	Leu	Gln	His	Glu	Thr	Gln	Met	Leu	Ile	Leu	Asp	Lys	Asn	Asp	Ser																											
		135						140				145																														
c	t	c	g	a	c	c	c	c	c	t	a	t	a	c	c	a	a	c	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	595				
Leu	Gly	Arg	Pro	Tyr	Val	Leu	Leu	Leu	Pro	Ile	Leu	Glu	Asn	Thr	Phe																											
		150						155				160																														
c	g	a	a	c	c	c	c	c	c	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	643				
Arg	Thr	Ser	Leu	Gln	Pro	Gly	Leu	Asn	Asp	His	Ile	Gly	Met	Ser	Val																											
								170																																		
g	a	a	c	c	c	c	c	c	c	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	691				
Glu	Ser	Gly	Ser	Thr	His	Val	Thr	Gly	Ser	Ser	Phe	Lys	Ala	Cys	Leu																											
								185																																		
t	a	c	c	c	c	c	c	c	c	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	739				
Tyr	Ile	His	Leu	Ser	Asn	Asp	Pro	Tyr	Ser	Ile	Leu	Lys	Glu	Ala	Val																											
								200																																		
a	a	a	a	a	a	a	a	a	a	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	787				
Lys	Val	Ile	Gln	Thr	Gln	Leu	Gly	Thr	Phe	Lys	Thr	Leu	Glu	Glu	Lys																											
								215																																		
a	a	a	a	a	a	a	a	a	a	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	835				
Thr	Ala	Pro	Ser	Ile	Ile	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala																											
								230																																		
t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	883				
Phe	Tyr	Leu	Lys	Val	His	Pro	Lys	Gly	Val	Trp	Glu	Gly	Val	Lys	Ser																											
								250																																		
c	t	c	g	a	c	c	c	c	c	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	931				
Leu	Thr	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Phe	Val	Ile	Ile	Asp	Asp	Gly																											
								265																																		
t	g	g	a	a	a	a	a	a	a	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	979				
Trp	Gln	Ser	Ile	Cys	His	Asp	Asp	Asp	Asp	Glu	Asp	Asp	Ser	Gly	Met																											
								280																																		
a	a	c	a	a	a	a	a	a	a	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1027				
Asn	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Val	Lys	Tyr																											
								295																																		
g	a	a	a	a	a	a	a	a	a	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1075				
Glu	Glu	Asn	Ser	Lys	Phe	Arg	Glu	Tyr	Glu	Asn	Pro	Glu	Asn	Gly	Gly																											
								310																																		
a	a	a	a	a	a	a	a	a	a	t	a	a	a	a	a	a	a	a	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1123				
Lys	Lys	Gly	Leu	Gly	Gly	Phe	Val	Arg	Asp	Leu	Lys	Glu	Lys	Glu	Phe																											
								330																																		
a	g	t	g	g	g	g	g	g	g	c	a	c	c	c	c	c	c	c	t	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1171				
Ser	Val	Glu	Ser	Val	Tyr	Val	Trp	His	Ala	Leu	Cys	Gly	Tyr	Trp	Gly																											
								345																																		

ggg gtt agg cct gga gtg cat ggg atg ccg aaa gct agg gtt gtt gtt	1219
Gly Val Arg Pro Gly Val His Gly Met Pro Lys Ala Arg Val Val Val	
360 365 370	
ccg aag gtg tct cag ggg ttg aag atg acg atg gag gat ttg gcg gtg	1267
Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met Glu Asp Leu Ala Val	
375 380 385	
gat aag att gtt gag aac ggt gtg ggg cta gtg ccg cca gat ttt gca	1315
Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val Pro Pro Asp Phe Ala	
390 395 400 405	
cat gag atg ttt gat ggg ctt cac tct cat ttg gag tcg gcg gga att	1363
His Glu Met Phe Asp Gly Leu His Ser His Leu Glu Ser Ala Gly Ile	
410 415 420	
gac ggt gtt aaa gtt gat gtt atc cat ctg ctt gag tta cta tca gag	1411
Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Leu Leu Ser Glu	
425 430 435	
gaa tat ggt gga cga gtt gag cta gca aga gct tat tac aaa gca cta	1459
Glu Tyr Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu	
440 445 450	
acc tca tca gtg aag aaa cat ttc aaa ggc aat ggt gta att gct agc	1507
Thr Ser Ser Val Lys Lys His Phe Lys Gly Asn Gly Val Ile Ala Ser	
455 460 465	
atg gag cat tgc aac gac ttc ttt ctc ctc ggc acc gaa gcc ata tcc	1555
Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu Ala Ile Ser	
470 475 480 485	
ctc ggc cgc gtc gga gat gat ttt tgg tgc tct gat cca tct ggt gat	1603
Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser Asp Pro Ser Gly Asp	
490 495 500	
cca aat ggt aca tat tgg ctc caa ggt tgt cac atg gta cat tgt gcc	1651
Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys Ala	
505 510 515	
tac aac agt tta tgg atg gga aat ttc att cag cca gat tgg gac atg	1699
Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp Trp Asp Met	
520 525 530	
ttt cag tcc act cat cct tgt gct gaa ttt cat gcc gcc tca cga gcc	1747
Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala Ser Arg Ala	
535 540 545	
ata tcc ggc gga cca att tat gtt agt gat tgt gtt ggt aat cac aat	1795
Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Cys Val Gly Asn His Asn	
550 555 560 565	
ttc aag ttg ctc aaa tct ctt gtt ttg ccc gat ggt tct atc ttg cgt	1843
Phe Lys Leu Leu Lys Ser Leu Val Leu Pro Asp Gly Ser Ile Leu Arg	
570 575 580	
tgt caa cat tac gca ctc cct aca aga gat tgc ttg ttt gaa gac cct	1891
Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp Pro	
585 590 595	

ttg cat aat ggc aaa aca atg ctg aaa att tgg aat ctc aac aaa tat	1939
Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys Tyr	
600 605 610	
aca ggt gtt ttg ggt ctt ttc aac tgc caa ggt ggt ggg tgg tgt cct	1987
Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp Cys Pro	
615 620 625	
gag gca cgg cga aac aag agt gta tct gaa ttt tca cgc gcg gtg aca	2035
Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe Ser Arg Ala Val Thr	
630 635 640 645	
tgt tat gca agt ccc gaa gac att gaa tgg tgc aat ggg aaa act cca	2083
Cys Tyr Ala Ser Pro Glu Asp Ile Glu Trp Cys Asn Gly Lys Thr Pro	
650 655 660	
atg agc acc aaa ggt gtg gat ttt ttt gct gtg tat ttt ttc aag gag	2131
Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val Tyr Phe Phe Lys Glu	
665 670 675	
aag aaa ttg agg ctc atg aag tgt tct gat aga ttg aaa gtt tcg ctt	2179
Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg Leu Lys Val Ser Leu	
680 685 690	
gag cca ttt agt ttt gag cta atg aca gtg tct cca gtg aaa gtg ttt	2227
Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser Pro Val Lys Val Phe	
695 700 705	
tcg aaa agg ttt ata cag ttt gca ccg att ggg tta gtg aac atg ctg	2275
Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu	
710 715 720 725	
aac tct ggt ggt gcg att cag tct ctg gag ttt gat gat aat gca agt	2323
Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe Asp Asp Asn Ala Ser	
730 735 740	
ttg gtc aag att ggg gtg aga ggt tgc ggg gag atg agc gtg ttt gcg	2371
Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Ser Val Phe Ala	
745 750 755	
tct gag aaa ccg gtt tgc tgc aaa att gat ggg gtt aag gtg aaa ttt	2419
Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly Val Lys Val Lys Phe	
760 765 770	
ctt tat gag gac aaa atg gca aga gtt caa att ctg tgg cct agt tct	2467
Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile Leu Trp Pro Ser Ser	
775 780 785	
tca aca ttg tct ttg gtc cag ttt tta ttt tgatccctag gaatcctatg	2517
Ser Thr Leu Ser Leu Val Gln Phe Leu Phe	
790 795	
cacgtgtctc tgtttacaag tactttatat aagtataata tgtatctatt tccattttta	2577
actgtcttta tgcaattagg tgggtcaatta gttatttggt tgtgaagtaa ctaacttgct	2637
tgtgttgtaa gcttataata tatgggtcaag ttcctcactt gtatatacct gttgtatgta	2697
taaattttac tatatatgac taacatcatt atcttgtgag caaaaaaaaa	2746

<210> 2  
 <211> 799  
 <212> PRT  
 <213> Vicia faba

<400> 2

Met	Ala	Pro	Pro	Ser	Ile	Thr	Lys	Thr	Ala	Thr	Leu	Gln	Asp	Val	Ile
1				5					10					15	
Ser	Thr	Ile	Asp	Ile	Gly	Asn	Gly	Asn	Ser	Pro	Leu	Phe	Ser	Ile	Thr
			20					25					30		
Leu	Asp	Gln	Ser	Arg	Asp	Phe	Leu	Ala	Asn	Gly	His	Pro	Phe	Leu	Thr
		35					40					45			
Gln	Val	Pro	Pro	Asn	Ile	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Ser	Ser
	50					55					60				
Phe	Leu	Asn	Leu	Lys	Ser	Asn	Lys	Asp	Thr	Ile	Pro	Asn	Asn	Asn	Asn
65				70						75					80
Thr	Met	Leu	Leu	Gln	Gln	Gly	Cys	Phe	Val	Gly	Phe	Asn	Ser	Thr	Glu
				85					90					95	
Pro	Lys	Ser	His	His	Val	Val	Pro	Leu	Gly	Lys	Leu	Lys	Gly	Ile	Lys
			100					105					110		
Phe	Met	Ser	Ile	Phe	Arg	Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val
	115						120					125			
Gly	Thr	Asn	Gly	Gln	Glu	Leu	Gln	His	Glu	Thr	Gln	Met	Leu	Ile	Leu
	130					135					140				
Asp	Lys	Asn	Asp	Ser	Leu	Gly	Arg	Pro	Tyr	Val	Leu	Leu	Leu	Pro	Ile
145					150					155					160
Leu	Glu	Asn	Thr	Phe	Arg	Thr	Ser	Leu	Gln	Pro	Gly	Leu	Asn	Asp	His
				165					170					175	
Ile	Gly	Met	Ser	Val	Glu	Ser	Gly	Ser	Thr	His	Val	Thr	Gly	Ser	Ser
			180					185					190		
Phe	Lys	Ala	Cys	Leu	Tyr	Ile	His	Leu	Ser	Asn	Asp	Pro	Tyr	Ser	Ile
		195					200					205			
Leu	Lys	Glu	Ala	Val	Lys	Val	Ile	Gln	Thr	Gln	Leu	Gly	Thr	Phe	Lys
	210					215					220				
Thr	Leu	Glu	Glu	Lys	Thr	Ala	Pro	Ser	Ile	Ile	Asp	Lys	Phe	Gly	Trp
225					230					235					240
Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Lys	Val	His	Pro	Lys	Gly	Val	Trp
				245					250					255	
Glu	Gly	Val	Lys	Ser	Leu	Thr	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Phe	Val
			260					265					270		
Ile	Ile	Asp	Asp	Gly	Trp	Gln	Ser	Ile	Cys	His	Asp	Asp	Asp	Asp	Glu
		275					280					285			
Asp	Asp	Ser	Gly	Met	Asn	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys

290	295	300
Arg Leu Val Lys Tyr Glu Glu Asn Ser Lys Phe Arg Glu Tyr Glu Asn 305 310 315 320		
Pro Glu Asn Gly Gly Lys Lys Gly Leu Gly Gly Phe Val Arg Asp Leu 325 330 335		
Lys Glu Glu Phe Gly Ser Val Glu Ser Val Tyr Val Trp His Ala Leu 340 345 350		
Cys Gly Tyr Trp Gly Gly Val Arg Pro Gly Val His Gly Met Pro Lys 355 360 365		
Ala Arg Val Val Val Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met 370 375 380		
Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val 385 390 395 400		
Pro Pro Asp Phe Ala His Glu Met Phe Asp Gly Leu His Ser His Leu 405 410 415		
Glu Ser Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu 420 425 430		
Glu Leu Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Arg Ala 435 440 445		
Tyr Tyr Lys Ala Leu Thr Ser Ser Val Lys Lys His Phe Lys Gly Asn 450 455 460		
Gly Val Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly 465 470 475 480		
Thr Glu Ala Ile Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser 485 490 495		
Asp Pro Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His 500 505 510		
Met Val His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln 515 520 525		
Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His 530 535 540		
Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Cys 545 550 555 560		
Val Gly Asn His Asn Phe Lys Leu Leu Lys Ser Leu Val Leu Pro Asp 565 570 575		
Gly Ser Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys 580 585 590		
Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp 595 600 605		
Asn Leu Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly 610 615 620		

Gly Gly Trp Cys Pro Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe  
 625 630 635 640  
 Ser Arg Ala Val Thr Cys Tyr Ala Ser Pro Glu Asp Ile Glu Trp Cys  
 645 650 655  
 Asn Gly Lys Thr Pro Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val  
 660 665 670  
 Tyr Phe Phe Lys Glu Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg  
 675 680 685  
 Leu Lys Val Ser Leu Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser  
 690 695 700  
 Pro Val Lys Val Phe Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly  
 705 710 715 720  
 Leu Val Asn Met Leu Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe  
 725 730 735  
 Asp Asp Asn Ala Ser Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu  
 740 745 750  
 Met Ser Val Phe Ala Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly  
 755 760 765  
 Val Lys Val Lys Phe Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile  
 770 775 780  
 Leu Trp Pro Ser Ser Ser Thr Leu Ser Leu Val Gln Phe Leu Phe  
 785 790 795

<210> 3  
 <211> 2498  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (62)..(2404)

<400> 3  
 ccaaaccata gcaaacctaa gcaccaaacc tctttctttc aagatccttg aattcagttcc 60

c atg gct cca agc ata agc aaa act gtg gaa cta aat tca ttt ggt ctt 109  
 Met Ala Pro Ser Ile Ser Lys Thr Val Glu Leu Asn Ser Phe Gly Leu  
 1 5 10 15

gtc aac ggt aat ttg cct ttg tcc ata acc cta gaa gga tca aat ttc 157  
 Val Asn Gly Asn Leu Pro Leu Ser Ile Thr Leu Glu Gly Ser Asn Phe  
 20 25 30

ctc gcc aac ggc cac cct ttt ctc acg gaa gtt ccc gaa aac ata ata 205  
 Leu Ala Asn Gly His Pro Phe Leu Thr Glu Val Pro Glu Asn Ile Ile  
 35 40 45

gtc acc cct tca ccc atc gac gcc aag agt agt aag aac aac gag gac 253  
 Val Thr Pro Ser Pro Ile Asp Ala Lys Ser Ser Lys Asn Asn Glu Asp

50					55					60						
gac	gac	gtc	gta	ggc	tgc	ttc	gtg	ggc	ttc	cac	gcg	gac	gag	ccc	aga	301
Asp	Asp	Val	Val	Gly	Cys	Phe	Val	Gly	Phe	His	Ala	Asp	Glu	Pro	Arg	
65					70					75					80	
agc	cga	cac	gtg	gct	tcc	ctg	ggg	aag	ctc	aga	gga	ata	aaa	ttc	atg	349
Ser	Arg	His	Val	Ala	Ser	Leu	Gly	Lys	Leu	Arg	Gly	Ile	Lys	Phe	Met	
				85					90					95		
agc	ata	ttc	cgg	ttt	aag	gtg	tgg	tgg	acc	act	cac	tgg	gtc	ggc	agc	397
Ser	Ile	Phe	Arg	Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Ser	
			100					105					110			
aac	gga	cac	gaa	ctg	gag	cac	gag	aca	cag	atg	atg	ctt	ctc	gac	aaa	445
Asn	Gly	His	Glu	Leu	Glu	His	Glu	Thr	Gln	Met	Met	Leu	Leu	Asp	Lys	
		115					120					125				
aac	gac	cag	ctc	gga	cgc	ccc	ttt	gtg	ttg	att	ctc	ccg	atc	ctc	caa	493
Asn	Asp	Gln	Leu	Gly	Arg	Pro	Phe	Val	Leu	Ile	Leu	Pro	Ile	Leu	Gln	
	130					135					140					
gcc	tcg	ttc	cga	gcc	tcc	ctg	caa	ccc	ggc	ttg	gat	gat	tac	gtg	gac	541
Ala	Ser	Phe	Arg	Ala	Ser	Leu	Gln	Pro	Gly	Leu	Asp	Asp	Tyr	Val	Asp	
145					150				155						160	
gtt	tgc	atg	gag	agc	ggg	tcg	aca	cgt	gtc	tgt	ggc	tcc	agc	ttc	ggg	589
Val	Cys	Met	Glu	Ser	Gly	Ser	Thr	Arg	Val	Cys	Gly	Ser	Ser	Phe	Gly	
				165					170					175		
agc	tgc	tta	tac	gtc	cac	gtt	ggc	cat	gac	ccg	tat	cag	ttg	ctt	aga	637
Ser	Cys	Leu	Tyr	Val	His	Val	Gly	His	Asp	Pro	Tyr	Gln	Leu	Leu	Arg	
			180					185					190			
gaa	gca	act	aaa	gtc	gtt	agg	atg	cat	ttg	ggg	acg	ttc	aag	ctt	ctc	685
Glu	Ala	Thr	Lys	Val	Val	Arg	Met	His	Leu	Gly	Thr	Phe	Lys	Leu	Leu	
		195					200					205				
gag	gag	aaa	acc	gcg	cca	gtg	atc	ata	gac	aag	ttt	ggc	tgg	tgt	aca	733
Glu	Glu	Lys	Thr	Ala	Pro	Val	Ile	Ile	Asp	Lys	Phe	Gly	Trp	Cys	Thr	
	210					215					220					
tgg	gac	gcg	ttt	tac	ttg	aag	gtg	cat	ccc	tca	ggc	gtg	tgg	gaa	ggg	781
Trp	Asp	Ala	Phe	Tyr	Leu	Lys	Val	His	Pro	Ser	Gly	Val	Trp	Glu	Gly	
225					230				235					240		
gtg	aaa	ggg	ttg	gtg	gag	gga	ggg	tgc	cct	cca	ggg	atg	gtc	cta	atc	829
Val	Lys	Gly	Leu	Val	Glu	Gly	Gly	Cys	Pro	Pro	Gly	Met	Val	Leu	Ile	
				245					250					255		
gac	gac	ggg	tgg	caa	gcc	att	tgt	cac	gac	gag	gac	ccc	ata	acg	gac	877
Asp	Asp	Gly	Trp	Gln	Ala	Ile	Cys	His	Asp	Glu	Asp	Pro	Ile	Thr	Asp	
			260					265					270			
caa	gag	ggc	atg	aag	cga	acc	tcc	gca	ggg	gag	caa	atg	cca	tgc	agg	925
Gln	Glu	Gly	Met	Lys	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	
		275					280					285				
ttg	gtg	aag	ttg	gag	gaa	aat	tac	aag	ttc	aga	cag	tat	tgt	agt	gga	973
Leu	Val	Lys	Leu	Glu	Glu	Asn	Tyr	Lys	Phe	Arg	Gln	Tyr	Cys	Ser	Gly	
	290					295					300					



aag gat tct gag aag ggt atg ggt gcc ttt gtt agg gac ttg aag gaa	1021
Lys Asp Ser Glu Lys Gly Met Gly Ala Phe Val Arg Asp Leu Lys Glu	
305 310 315 320	
cag ttt agg agc gtg gag cag gtg tat gtg tgg cac gcg ctt tgt ggg	1069
Gln Phe Arg Ser Val Glu Gln Val Tyr Val Trp His Ala Leu Cys Gly	
325 330 335	
tat tgg ggt ggg gtc aga ccc aag gtt ccg ggc atg ccc cag gct aag	1117
Tyr Trp Gly Gly Val Arg Pro Lys Val Pro Gly Met Pro Gln Ala Lys	
340 345 350	
gtt gtc act ccg aag ctg tcc aat gga cta aaa ttg aca atg aag gat	1165
Val Val Thr Pro Lys Leu Ser Asn Gly Leu Lys Leu Thr Met Lys Asp	
355 360 365	
tta gcg gtg gat aag atc gtc agt aac gga gtt gga ctg gtg cca cca	1213
Leu Ala Val Asp Lys Ile Val Ser Asn Gly Val Gly Leu Val Pro Pro	
370 375 380	
cac ctg gct cac ctt ttg tac gag ggg ctc cac tcc cgt ttg gaa tct	1261
His Leu Ala His Leu Leu Tyr Glu Gly Leu His Ser Arg Leu Glu Ser	
385 390 395 400	
gcg ggt att gac ggt gtt aag gtt gac gtt ata cac ttg ctc gag atg	1309
Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Met	
405 410 415	
cta tcc gag gaa tac ggt ggc cgt gtt gag cta gcc aaa gct tat tac	1357
Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Lys Ala Tyr Tyr	
420 425 430	
aaa gcg ctc act gct tcg gtg aag aag cat ttc aaa ggc aat ggg gtc	1405
Lys Ala Leu Thr Ala Ser Val Lys Lys His Phe Lys Gly Asn Gly Val	
435 440 445	
att gcg agc atg gag cat tgt aat gac ttc ttt ctc ctt ggt acc gaa	1453
Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu	
450 455 460	
gcc ata gcc ctt ggg cgc gta gga gat gat ttt tgg tgc act gat ccc	1501
Ala Ile Ala Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro	
465 470 475 480	
tct gga gat cca aat ggc acg tat tgg ctc caa ggg tgt cac atg gtg	1549
Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val	
485 490 495	
cac tgt gcc tac aac agc ttg tgg atg ggg aat ttt att cag ccg gat	1597
His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp	
500 505 510	
tgg gac atg ttc cag tcc act cac cct tgt gcc gaa ttc cat gcg gcc	1645
Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala	
515 520 525	
tct agg gcc atc tct ggt gga cca gtt tac gtt agt gat tgt gtt gga	1693
Ser Arg Ala Ile Ser Gly Gly Pro Val Tyr Val Ser Asp Cys Val Gly	
530 535 540	

aag cac aac ttc aag ttg ctc aag agc ctc gct ttg cct gat ggg acg	1741
Lys His Asn Phe Lys Leu Leu Lys Ser Leu Ala Leu Pro Asp Gly Thr	
545 550 555 560	
att ttg cgt tgt caa cac tat gca ctc ccc aca cga gac tgt ttg ttt	1789
Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe	
565 570 575	
gaa gac ccc ttg cat gat ggg aag aca atg ctc aaa att tgg aat ctc	1837
Glu Asp Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu	
580 585 590	
aac aaa tat aca ggt gtt ttg ggt cta ttt aat tgc caa gga ggt ggg	1885
Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly	
595 600 605	
tgg tgt ccc gta act agg aga aac aag agt gcc tct gaa ttt tca caa	1933
Trp Cys Pro Val Thr Arg Arg Asn Lys Ser Ala Ser Glu Phe Ser Gln	
610 615 620	
act gtg aca tgc tta gcg agt cct caa gac att gaa tgg agc aat ggg	1981
Thr Val Thr Cys Leu Ala Ser Pro Gln Asp Ile Glu Trp Ser Asn Gly	
625 630 635 640	
aaa agc cca ata tgc ata aaa ggg atg aat gtg ttt gct gta tat ttg	2029
Lys Ser Pro Ile Cys Ile Lys Gly Met Asn Val Phe Ala Val Tyr Leu	
645 650 655	
ttc aag gac cac aaa cta aag ctc atg aag gca tca gag aaa ttg gaa	2077
Phe Lys Asp His Lys Leu Lys Leu Met Lys Ala Ser Glu Lys Leu Glu	
660 665 670	
gtt tca ctt gag cca ttt act ttt gag cta ttg aca gtg tct cca gtg	2125
Val Ser Leu Glu Pro Phe Thr Phe Glu Leu Leu Thr Val Ser Pro Val	
675 680 685	
att gtg ctg tca aaa aag tta att caa ttt gct cca att gga tta gtg	2173
Ile Val Leu Ser Lys Lys Leu Ile Gln Phe Ala Pro Ile Gly Leu Val	
690 695 700	
aac atg ctt aac act ggt ggt gcc att cag tcc atg gag ttt gac aac	2221
Asn Met Leu Asn Thr Gly Gly Ala Ile Gln Ser Met Glu Phe Asp Asn	
705 710 715 720	
cac ata gat gtg gtc aaa att ggg gtt agg ggt tgt ggg gag atg aag	2269
His Ile Asp Val Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Lys	
725 730 735	
gtg ttt gca tca gag aaa cca gtt agt tgc aaa cta gat ggg gta gtt	2317
Val Phe Ala Ser Glu Lys Pro Val Ser Cys Lys Leu Asp Gly Val Val	
740 745 750	
gta aaa ttt gat tat gag gat aaa atg ctg aga gtg caa gtt ccc tgg	2365
Val Lys Phe Asp Tyr Glu Asp Lys Met Leu Arg Val Gln Val Pro Trp	
755 760 765	
cct agt gct tca aaa ttg tca atg gtt gag ttt tta ttt tgatccctga	2414
Pro Ser Ala Ser Lys Leu Ser Met Val Glu Phe Leu Phe	
770 775 780	
aggtgaattt gggatactat gatgtttgac tctcttttta agtaataaga gtcataattt	2474

tctgttgtaa aaaaaaaaaa aaaa

2498

<210> 4

<211> 781

<212> PRT

<213> Glycine max

<400> 4

Met	Ala	Pro	Ser	Ile	Ser	Lys	Thr	Val	Glu	Leu	Asn	Ser	Phe	Gly	Leu	
1				5					10					15		
Val	Asn	Gly	Asn	Leu	Pro	Leu	Ser	Ile	Thr	Leu	Glu	Gly	Ser	Asn	Phe	
			20					25					30			
Leu	Ala	Asn	Gly	His	Pro	Phe	Leu	Thr	Glu	Val	Pro	Glu	Asn	Ile	Ile	
		35					40					45				
Val	Thr	Pro	Ser	Pro	Ile	Asp	Ala	Lys	Ser	Ser	Lys	Asn	Asn	Glu	Asp	
	50					55					60					
Asp	Asp	Val	Val	Gly	Cys	Phe	Val	Gly	Phe	His	Ala	Asp	Glu	Pro	Arg	
65					70					75					80	
Ser	Arg	His	Val	Ala	Ser	Leu	Gly	Lys	Leu	Arg	Gly	Ile	Lys	Phe	Met	
			85						90					95		
Ser	Ile	Phe	Arg	Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Ser	
			100					105					110			
Asn	Gly	His	Glu	Leu	Glu	His	Glu	Thr	Gln	Met	Met	Leu	Leu	Asp	Lys	
		115					120					125				
Asn	Asp	Gln	Leu	Gly	Arg	Pro	Phe	Val	Leu	Ile	Leu	Pro	Ile	Leu	Gln	
	130					135					140					
Ala	Ser	Phe	Arg	Ala	Ser	Leu	Gln	Pro	Gly	Leu	Asp	Asp	Tyr	Val	Asp	
145					150					155					160	
Val	Cys	Met	Glu	Ser	Gly	Ser	Thr	Arg	Val	Cys	Gly	Ser	Ser	Phe	Gly	
			165						170					175		
Ser	Cys	Leu	Tyr	Val	His	Val	Gly	His	Asp	Pro	Tyr	Gln	Leu	Leu	Arg	
		180						185					190			
Glu	Ala	Thr	Lys	Val	Val	Arg	Met	His	Leu	Gly	Thr	Phe	Lys	Leu	Leu	
		195					200					205				
Glu	Glu	Lys	Thr	Ala	Pro	Val	Ile	Ile	Asp	Lys	Phe	Gly	Trp	Cys	Thr	
	210					215					220					
Trp	Asp	Ala	Phe	Tyr	Leu	Lys	Val	His	Pro	Ser	Gly	Val	Trp	Glu	Gly	
225					230					235					240	
Val	Lys	Gly	Leu	Val	Glu	Gly	Gly	Cys	Pro	Pro	Gly	Met	Val	Leu	Ile	
			245						250					255		
Asp	Asp	Gly	Trp	Gln	Ala	Ile	Cys	His	Asp	Glu	Asp	Pro	Ile	Thr	Asp	
		260						265					270			

Gln Glu Gly Met Lys Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg  
 275 280 285  
 Leu Val Lys Leu Glu Glu Asn Tyr Lys Phe Arg Gln Tyr Cys Ser Gly  
 290 295 300  
 Lys Asp Ser Glu Lys Gly Met Gly Ala Phe Val Arg Asp Leu Lys Glu  
 305 310 315 320  
 Gln Phe Arg Ser Val Glu Gln Val Tyr Val Trp His Ala Leu Cys Gly  
 325 330 335  
 Tyr Trp Gly Gly Val Arg Pro Lys Val Pro Gly Met Pro Gln Ala Lys  
 340 345 350  
 Val Val Thr Pro Lys Leu Ser Asn Gly Leu Lys Leu Thr Met Lys Asp  
 355 360 365  
 Leu Ala Val Asp Lys Ile Val Ser Asn Gly Val Gly Leu Val Pro Pro  
 370 375 380  
 His Leu Ala His Leu Leu Tyr Glu Gly Leu His Ser Arg Leu Glu Ser  
 385 390 395 400  
 Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Met  
 405 410 415  
 Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Lys Ala Tyr Tyr  
 420 425 430  
 Lys Ala Leu Thr Ala Ser Val Lys Lys His Phe Lys Gly Asn Gly Val  
 435 440 445  
 Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu  
 450 455 460  
 Ala Ile Ala Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro  
 465 470 475 480  
 Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val  
 485 490 495  
 His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp  
 500 505 510  
 Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala  
 515 520 525  
 Ser Arg Ala Ile Ser Gly Gly Pro Val Tyr Val Ser Asp Cys Val Gly  
 530 535 540  
 Lys His Asn Phe Lys Leu Leu Lys Ser Leu Ala Leu Pro Asp Gly Thr  
 545 550 555 560  
 Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe  
 565 570 575  
 Glu Asp Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu  
 580 585 590  
 Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly

595					600					605					
Trp	Cys	Pro	Val	Thr	Arg	Arg	Asn	Lys	Ser	Ala	Ser	Glu	Phe	Ser	Gln
610						615					620				
Thr	Val	Thr	Cys	Leu	Ala	Ser	Pro	Gln	Asp	Ile	Glu	Trp	Ser	Asn	Gly
625					630					635					640
Lys	Ser	Pro	Ile	Cys	Ile	Lys	Gly	Met	Asn	Val	Phe	Ala	Val	Tyr	Leu
				645					650					655	
Phe	Lys	Asp	His	Lys	Leu	Lys	Leu	Met	Lys	Ala	Ser	Glu	Lys	Leu	Glu
			660					665					670		
Val	Ser	Leu	Glu	Pro	Phe	Thr	Phe	Glu	Leu	Leu	Thr	Val	Ser	Pro	Val
			675				680					685			
Ile	Val	Leu	Ser	Lys	Lys	Leu	Ile	Gln	Phe	Ala	Pro	Ile	Gly	Leu	Val
	690					695					700				
Asn	Met	Leu	Asn	Thr	Gly	Gly	Ala	Ile	Gln	Ser	Met	Glu	Phe	Asp	Asn
705					710					715					720
His	Ile	Asp	Val	Val	Lys	Ile	Gly	Val	Arg	Gly	Cys	Gly	Glu	Met	Lys
				725					730					735	
Val	Phe	Ala	Ser	Glu	Lys	Pro	Val	Ser	Cys	Lys	Leu	Asp	Gly	Val	Val
			740					745					750		
Val	Lys	Phe	Asp	Tyr	Glu	Asp	Lys	Met	Leu	Arg	Val	Gln	Val	Pro	Trp
	755						760					765			
Pro	Ser	Ala	Ser	Lys	Leu	Ser	Met	Val	Glu	Phe	Leu	Phe			
	770					775					780				

<210> 5  
 <211> 1762  
 <212> DNA  
 <213> *Stachys sieboldii*

<220>  
 <221> CDS  
 <222> (2) .. (1759)

<400> 5

g aca aac ggg tcg gat ctt gag cgg gaa act caa ata gtc gtg ctc gac 49														
Thr Asn Gly Ser Asp Leu Glu Arg Glu Thr Gln Ile Val Val Leu Asp														
1					5					10				15
aag tcc gac gac agg ccc tac atc gtg ctg ctt ccg ctc atc gag ggg 97														
Lys Ser Asp Asp Arg Pro Tyr Ile Val Leu Leu Pro Leu Ile Glu Gly														
			20					25					30	
cag ttt cgg gct tcc ctt cag ccc ggt gtg gat gat ttt atc gat att 145														
Gln Phe Arg Ala Ser Leu Gln Pro Gly Val Asp Asp Phe Ile Asp Ile														
			35				40					45		
tgt gtc gaa agc ggg tca acc aag gtc aac gag tcc tcg ttc cgt gct 193														
Cys Val Glu Ser Gly Ser Thr Lys Val Asn Glu Ser Ser Phe Arg Ala														
		50				55					60			

tcg ctc tac atg cac gcc ggt gat gac cct ttt acc ctg gtg aag gac	241
Ser Leu Tyr Met His Ala Gly Asp Asp Pro Phe Thr Leu Val Lys Asp	
65 70 75 80	
gcc gtg aag gtg gcg cgc cac cac ctc ggg acg ttc agg ctg ctg gag	289
Ala Val Lys Val Ala Arg His His Leu Gly Thr Phe Arg Leu Leu Glu	
85 90 95	
gag aaa act ccg ccg ggg atc gtc gac aaa ttc ggg tgg tgc acg tgg	337
Glu Lys Thr Pro Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp	
100 105 110	
gat gcg ttc tac ctc aac gtc cag ccc cac ggc gtt atg gag ggc gtg	385
Asp Ala Phe Tyr Leu Asn Val Gln Pro His Gly Val Met Glu Gly Val	
115 120 125	
cag ggg ctg gtt gac ggc gga tgt ccg ccg ggg ctg gtg ttg atc gac	433
Gln Gly Leu Val Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp	
130 135 140	
gac ggg tgg cag tcc att tgt cac gac aac gac gcg ctc acc acc gag	481
Asp Gly Trp Gln Ser Ile Cys His Asp Asn Asp Ala Leu Thr Thr Glu	
145 150 155 160	
ggg atg ggg aga acc tcc gcc gga gag caa atg ccc tgc agg ttg atc	529
Gly Met Gly Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Ile	
165 170 175	
aag ttt gag gag aat tac aag ttc agg gag tac gag agc ccg aat aaa	577
Lys Phe Glu Glu Asn Tyr Lys Phe Arg Glu Tyr Glu Ser Pro Asn Lys	
180 185 190	
act ggg ccg ggc ccg aat acg ggg atg ggg gcc ttt att cgt gac atg	625
Thr Gly Pro Gly Pro Asn Thr Gly Met Gly Ala Phe Ile Arg Asp Met	
195 200 205	
aag gac aat ttc aag agt gtg gac tac gtg tac gtg tgg cat gcg ttg	673
Lys Asp Asn Phe Lys Ser Val Asp Tyr Val Tyr Val Trp His Ala Leu	
210 215 220	
tgt ggt tat tgg ggc ggg ctc agg ccc aat gtt ccg ggc ctg ccc gag	721
Cys Gly Tyr Trp Gly Gly Leu Arg Pro Asn Val Pro Gly Leu Pro Glu	
225 230 235 240	
gct aag ctc att gag ccc aaa ctg act cct ggg ctt aag acc acc atg	769
Ala Lys Leu Ile Glu Pro Lys Leu Thr Pro Gly Leu Lys Thr Thr Met	
245 250 255	
gaa gat ttg gct gtt gat aag att gtc aac aat ggc gtg ggt ctg gtc	817
Glu Asp Leu Ala Val Asp Lys Ile Val Asn Asn Gly Val Gly Leu Val	
260 265 270	
cca ccg gag ttt gtt gaa caa atg tat gaa gga tta cat tca cat ctc	865
Pro Pro Glu Phe Val Glu Gln Met Tyr Glu Gly Leu His Ser His Leu	
275 280 285	
gaa tct gtg ggg att gat gga gtc aaa gtt gac gtc atc cat ttg ttg	913
Glu Ser Val Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu	
290 295 300	

gaa atg ttg tgt gaa gac tat ggt ggg aga gtg gac tta gcc aag gct	961
Glu Met Leu Cys Glu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala	
305 310 315 320	
tat tac aag gcc tta tca agc tca gtt aac aac cac ttc aac ggc aac	1009
Tyr Tyr Lys Ala Leu Ser Ser Ser Val Asn Asn His Phe Asn Gly Asn	
325 330 335	
ggc gtc atc gct ggc ctg gag cac tgc aat gac ttc atg ttt ctc gga	1057
Gly Val Ile Ala Gly Leu Glu His Cys Asn Asp Phe Met Phe Leu Gly	
340 345 350	
acc gag gcc att acc ttg ggt cgt gtc ggg gat gat ttt tgg tgc act	1105
Thr Glu Ala Ile Thr Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr	
355 360 365	
gat cca tct gga gat ccc aat ggc acg ttc tgg ttg caa ggg tgt cac	1153
Asp Pro Ser Gly Asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His	
370 375 380	
atg gtg cac tgc gcc tac aac agc ata tgg atg ggt aat ttc atc cac	1201
Met Val His Cys Ala Tyr Asn Ser Ile Trp Met Gly Asn Phe Ile His	
385 390 395 400	
cct gat tgg gac atg ttt caa tcg act cac cct tgc gct gaa ttc cac	1249
Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His	
405 410 415	
gct gcc tca cga gcc atc tcc ggc ggg ccc att tac gtc agt gac tcg	1297
Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser	
420 425 430	
gtc gga aag cac aac ttc gag ctc ctt agg agc ctc gtt ctt ccc gat	1345
Val Gly Lys His Asn Phe Glu Leu Leu Arg Ser Leu Val Leu Pro Asp	
435 440 445	
ggc tcc atc ctc cgt tgt gat tac tac gcg ctt ccg act cgc gat tgc	1393
Gly Ser Ile Leu Arg Cys Asp Tyr Tyr Ala Leu Pro Thr Arg Asp Cys	
450 455 460	
ctc ttt gaa gat cca ctt cac aat ggc aag act atg ctc aaa att tgg	1441
Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp	
465 470 475 480	
aat tat aac aag ttc acc gga gtt gtc gga act ttc aac tgc caa ggt	1489
Asn Tyr Asn Lys Phe Thr Gly Val Val Gly Thr Phe Asn Cys Gln Gly	
485 490 495	
ggc ggg tgg agc cgg gaa gtg cgt cgc aac caa tgc gct gcc gag tat	1537
Gly Gly Trp Ser Arg Glu Val Arg Arg Asn Gln Cys Ala Ala Glu Tyr	
500 505 510	
tcc cac gcc gtc tcc tct agc gct ggt ccg agt gac att gag tgg aag	1585
Ser His Ala Val Ser Ser Ser Ala Gly Pro Ser Asp Ile Glu Trp Lys	
515 520 525	
caa gga acg agt ccg atc gac gtc gac ggc gtc aaa aca ttc gcg ttg	1633
Gln Gly Thr Ser Pro Ile Asp Val Asp Gly Val Lys Thr Phe Ala Leu	
530 535 540	
tac cta ttc cac gag aag aaa ctc gtc ctt tct aag cca tca gac aaa	1681

Tyr Leu Phe His Glu Lys Lys Leu Val Leu Ser Lys Pro Ser Asp Lys  
 545 550 555 560

atc gac atc acg ctt gag ccc ttc gat ttt gag ctg ata acc gtt tct 1729  
 Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val Ser  
 565 570 575

cca gtc aaa act cta gcc aat tgc acc gtc caa 1762  
 Pro Val Lys Thr Leu Ala Asn Cys Thr Val  
 580 585

<210> 6  
 <211> 586  
 <212> PRT  
 <213> Stachys sieboldii

<400> 6  
 Thr Asn Gly Ser Asp Leu Glu Arg Glu Thr Gln Ile Val Val Leu Asp  
 1 5 10 15

Lys Ser Asp Asp Arg Pro Tyr Ile Val Leu Leu Pro Leu Ile Glu Gly  
 20 25 30

Gln Phe Arg Ala Ser Leu Gln Pro Gly Val Asp Asp Phe Ile Asp Ile  
 35 40 45

Cys Val Glu Ser Gly Ser Thr Lys Val Asn Glu Ser Ser Phe Arg Ala  
 50 55 60

Ser Leu Tyr Met His Ala Gly Asp Asp Pro Phe Thr Leu Val Lys Asp  
 65 70 75 80

Ala Val Lys Val Ala Arg His His Leu Gly Thr Phe Arg Leu Leu Glu  
 85 90 95

Glu Lys Thr Pro Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp  
 100 105 110

Asp Ala Phe Tyr Leu Asn Val Gln Pro His Gly Val Met Glu Gly Val  
 115 120 125

Gln Gly Leu Val Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp  
 130 135 140

Asp Gly Trp Gln Ser Ile Cys His Asp Asn Asp Ala Leu Thr Thr Glu  
 145 150 155 160

Gly Met Gly Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Ile  
 165 170 175

Lys Phe Glu Glu Asn Tyr Lys Phe Arg Glu Tyr Glu Ser Pro Asn Lys  
 180 185 190

Thr Gly Pro Gly Pro Asn Thr Gly Met Gly Ala Phe Ile Arg Asp Met  
 195 200 205

Lys Asp Asn Phe Lys Ser Val Asp Tyr Val Tyr Val Trp His Ala Leu  
 210 215 220

Cys Gly Tyr Trp Gly Gly Leu Arg Pro Asn Val Pro Gly Leu Pro Glu



225		230		235		240
Ala Lys Leu Ile	Glu Pro Lys Leu Thr	Pro Gly Leu Lys Thr	Thr Met			
	245		250			255
Glu Asp Leu Ala	Val Asp Lys Ile	Val Asn Asn Gly	Val Gly Leu Val			
	260		265			270
Pro Pro Glu Phe	Val Glu Gln Met	Tyr Glu Gly Leu	His Ser His Leu			
	275		280			285
Glu Ser Val Gly	Ile Asp Gly Val	Lys Val Asp Val	Ile His Leu Leu			
	290		295			300
Glu Met Leu Cys	Glu Asp Tyr Gly	Gly Arg Val Asp	Leu Ala Lys Ala			
	305		310			315
Tyr Tyr Lys Ala	Leu Ser Ser Ser	Val Asn Asn His	Phe Asn Gly Asn			
	325		330			335
Gly Val Ile Ala	Gly Leu Glu His	Cys Asn Asp Phe	Met Phe Leu Gly			
	340		345			350
Thr Glu Ala Ile	Thr Leu Gly Arg	Val Gly Asp Asp	Phe Trp Cys Thr			
	355		360			365
Asp Pro Ser Gly	Asp Pro Asn Gly	Thr Phe Trp Leu	Gln Gly Cys His			
	370		375			380
Met Val His Cys	Ala Tyr Asn Ser	Ile Trp Met Gly	Asn Phe Ile His			
	385		390			395
Pro Asp Trp Asp	Met Phe Gln Ser	Thr His Pro Cys	Ala Glu Phe His			
	405		410			415
Ala Ala Ser Arg	Ala Ile Ser Gly	Gly Pro Ile Tyr	Val Ser Asp Ser			
	420		425			430
Val Gly Lys His	Asn Phe Glu Leu	Leu Arg Ser Leu	Val Leu Pro Asp			
	435		440			445
Gly Ser Ile Leu	Arg Cys Asp Tyr	Tyr Ala Leu Pro	Thr Arg Asp Cys			
	450		455			460
Leu Phe Glu Asp	Pro Leu His Asn	Gly Lys Thr Met	Leu Lys Ile Trp			
	465		470			475
Asn Tyr Asn Lys	Phe Thr Gly Val	Val Gly Thr Phe	Asn Cys Gln Gly			
	485		490			495
Gly Gly Trp Ser	Arg Glu Val Arg	Arg Asn Gln Cys	Ala Ala Glu Tyr			
	500		505			510
Ser His Ala Val	Ser Ser Ser Ala	Gly Pro Ser Asp	Ile Glu Trp Lys			
	515		520			525
Gln Gly Thr Ser	Pro Ile Asp Val	Asp Gly Val Lys	Thr Phe Ala Leu			
	530		535			540
Tyr Leu Phe His	Glu Lys Lys Leu	Val Leu Ser Lys	Pro Ser Asp Lys			
	545		550			555
						560

Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val Ser  
565 570 575

Pro Val Lys Thr Leu Ala Asn Cys Thr Val  
580 585

<210> 7  
<211> 993  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (2) .. (814)

<400> 7

c cag tcc acg cac ccc tgc gcc gcc ttc cac gcc gcg tcc cgc gcc atc 49  
Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg Ala Ile  
1 5 10 15

tcc ggc ggg ccc atc tac gtc agc gac tgc gtg ggg cag cac gac ttc 97  
Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Gln His Asp Phe  
20 25 30

gcg ctg ctc cgc cgc ctg gcg ctc ccc gac ggc acc gtc ctc cgg tgc 145  
Ala Leu Leu Arg Arg Leu Ala Leu Pro Asp Gly Thr Val Leu Arg Cys  
35 40 45

gag ggc cac gcg ctg ccc acg cgc gac tgc ctc ttc gcc gac ccg ctc 193  
Glu Gly His Ala Leu Pro Thr Arg Asp Cys Leu Phe Ala Asp Pro Leu  
50 55 60

cac gac ggc cgg acc gtg ctc aag atc tgg aac gtg aac cgc ttc gcc 241  
His Asp Gly Arg Thr Val Leu Lys Ile Trp Asn Val Asn Arg Phe Ala  
65 70 75 80

ggc gtc gtc ggc gcc ttc aac tgc cag ggc ggc ggg tgg agc ccc gag 289  
Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro Glu  
85 90 95

gcg cgg cgg aac aag tgc ttc tgc gag ttc tcc gtg ccc ctg gcc gcg 337  
Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala Ala  
100 105 110

cgc gcc tgc ccg tcc gac gtc gag tgg aag agc ggc aag gcg ggg cca 385  
Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly Pro  
115 120 125

ggc gtc agc gtc aag gac gtc tcc cag ttc gcc gtg tac gcg gtc gag 433  
Gly Val Ser Val Lys Asp Val Ser Gln Phe Ala Val Tyr Ala Val Glu  
130 135 140

gcc agg acg ctg cag ctg ctg cgc ccc gac gag ggc gtc gac ctc acg 481  
Ala Arg Thr Leu Gln Leu Leu Arg Pro Asp Glu Gly Val Asp Leu Thr  
145 150 155 160

ctg cag ccc ttc acc tac gag ctc ttc gtc gtt gcc ccc gtg cgc gtc 529  
Leu Gln Pro Phe Thr Tyr Glu Leu Phe Val Val Ala Pro Val Arg Val  
165 170 175

atc tcg cat gag cgg gcc atc aag ttc gcg ccc atc gga ctc gcc aac 577  
 Ile Ser His Glu Arg Ala Ile Lys Phe Ala Pro Ile Gly Leu Ala Asn  
 180 185 190

atg ctc aac acc gcc ggc gcc gtg cag gcg ttc gag gcc aag aaa gat 625  
 Met Leu Asn Thr Ala Gly Ala Val Gln Ala Phe Glu Ala Lys Lys Asp  
 195 200 205

gct agc ggc gtc acg gca gag gtg ttc gtg aag ggc gca ggg gag ctg 673  
 Ala Ser Gly Val Thr Ala Glu Val Phe Val Lys Gly Ala Gly Glu Leu  
 210 215 220

gtg gcg tac tcg tcg gcg acg ccc agg ctc tgc aag gtg aac ggc gac 721  
 Val Ala Tyr Ser Ser Ala Thr Pro Arg Leu Cys Lys Val Asn Gly Asp  
 225 230 235 240

gag gcc gag ttc acg tac aag gac ggc gtg gtc acc gtc gac gtg ccg 769  
 Glu Ala Glu Phe Thr Tyr Lys Asp Gly Val Val Thr Val Asp Val Pro  
 245 250 255

tgg tcg ggg tcg tcg tcg aag ctg tgt tgc gtc cag tac gtc tac 814  
 Trp Ser Gly Ser Ser Ser Lys Leu Cys Cys Val Gln Tyr Val Tyr  
 260 265 270

tgagccggac gggccgatga ctctgcgtct ctgctccctg ctggcctgct caggacataa 874  
 tctaattgttt agagcttacc aggttttaca gctctatcag tttacttttg tttttctgct 934  
 cttcgttttt taagaattat ttctattgtg tgaattaatg agtgctttcc ttctaaaaa 993

<210> 8  
 <211> 271  
 <212> PRT  
 <213> Zea mays

<400> 8  
 Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg Ala Ile  
 1 5 10 15

Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Gln His Asp Phe  
 20 25 30

Ala Leu Leu Arg Arg Leu Ala Leu Pro Asp Gly Thr Val Leu Arg Cys  
 35 40 45

Glu Gly His Ala Leu Pro Thr Arg Asp Cys Leu Phe Ala Asp Pro Leu  
 50 55 60

His Asp Gly Arg Thr Val Leu Lys Ile Trp Asn Val Asn Arg Phe Ala  
 65 70 75 80

Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro Glu  
 85 90 95

Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala Ala  
 100 105 110

Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly Pro  
 115 120 125

Gly Val Ser Val Lys Asp Val Ser Gln Phe Ala Val Tyr Ala Val Glu  
 130 135 140  
 Ala Arg Thr Leu Gln Leu Leu Arg Pro Asp Glu Gly Val Asp Leu Thr  
 145 150 155 160  
 Leu Gln Pro Phe Thr Tyr Glu Leu Phe Val Val Ala Pro Val Arg Val  
 165 170 175  
 Ile Ser His Glu Arg Ala Ile Lys Phe Ala Pro Ile Gly Leu Ala Asn  
 180 185 190  
 Met Leu Asn Thr Ala Gly Ala Val Gln Ala Phe Glu Ala Lys Lys Asp  
 195 200 205  
 Ala Ser Gly Val Thr Ala Glu Val Phe Val Lys Gly Ala Gly Glu Leu  
 210 215 220  
 Val Ala Tyr Ser Ser Ala Thr Pro Arg Leu Cys Lys Val Asn Gly Asp  
 225 230 235 240  
 Glu Ala Glu Phe Thr Tyr Lys Asp Gly Val Val Thr Val Asp Val Pro  
 245 250 255  
 Trp Ser Gly Ser Ser Ser Lys Leu Cys Cys Val Gln Tyr Val Tyr  
 260 265 270

<210> 9  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 1 (from list 1)

<400> 9  
 aattttcaag catagccaag ttaaccacct

30

<210> 10  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 2 (from list 1)

<400> 10  
 gtcacaaga taatgatgtt agtc

24

<210> 11  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 3 (from list 1)

<400> 11  
atacaagtga ggaacttgac ca 22

<210> 12  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 4 (from list 1)

<400> 12  
ccaaaccata gcaaacctaa gcac 24

<210> 13  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 5 (from list 1)

<400> 13  
acaacagaaa aatatgactc ttattact 28

<210> 14  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 6 (from list 1)

<400> 14  
aaaagagagt caaacatcat agtatc 26

<210> 15  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 1 (from list 2)

<400> 15  
atggcaccac caagcataac caaaaactgc 29

<210> 16  
<211> 43

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 2 (from list 2)

<400> 16

atggcaccac caagcataac caaaactgca accctccaag acg

43

<210> 17

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 3 (from list 2)

<400> 17

tcaaaataaa aactggacca aagac

25

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 4 (from list 2)

<400> 18

tcaaaataaa aactggacca aagacaatgt

30

<210> 19

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 5 (from list 2)

<400> 19

atggctccaa gcataagcaa aactg

25

<210> 20

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 6 (from list 2)

<400> 20

atggctccaa gcataagcaa aactgtggaa ct

32

<210> 21  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 7 (from list 2)

<400> 21  
 tcaaaataaaa aactcaacca ttgac 25

<210> 22  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 8 (from list 2)

<400> 22  
 tcaaaataaaa aactcaacca ttgacaattt tgaagcact 39

<210> 23  
 <211> 20  
 <212> PRT  
 <213> Vicia faba

<400> 23  
 Gly Ile Lys Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr  
 1 5 10 15  
 His Trp Val Gly  
 20

<210> 24  
 <211> 14  
 <212> PRT  
 <213> Vicia faba

<400> 24  
 Ile Ile Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr  
 1 5 10

<210> 25  
 <211> 15  
 <212> PRT  
 <213> Vicia faba

<400> 25  
 Gly Gly Cys Pro Pro Gly Phe Val Ile Ile Asp Asp Gly Trp Gln  
 1 5 10 15

<210> 26  
<211> 17  
<212> PRT  
<213> Vicia faba

<400> 26  
Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Val Lys Tyr Glu Glu  
1 5 10 15

Asn

<210> 27  
<211> 16  
<212> PRT  
<213> Vicia faba

<400> 27  
Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly Gly Val Arg Pro  
1 5 10 15

<210> 28  
<211> 20  
<212> PRT  
<213> Vicia faba

<400> 28  
Thr Met Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly  
1 5 10 15

Leu Val Pro Pro  
20

<210> 29  
<211> 23  
<212> PRT  
<213> Vicia faba

<400> 29  
Gly Leu His Ser His Leu Glu Ser Ala Gly Ile Asp Gly Val Lys Val  
1 5 10 15

Asp Val Ile His Leu Leu Glu  
20

<210> 30  
<211> 14  
<212> PRT  
<213> Vicia faba

<400> 30  
Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu  
1 5 10

<210> 31  
<211> 12



<212> PRT  
<213> Vicia faba

<400> 31  
Val Lys Lys His Phe Lys Gly Asn Gly Val Ile Ala  
1 5 10

<210> 32  
<211> 46  
<212> PRT  
<213> Vicia faba

<400> 32  
Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu Ala Ile Ser Leu  
1 5 10 15  
Gly Arg Val Gly Asp Asp Phe Trp Cys Ser Asp Pro Ser Gly Asp Pro  
20 25 30  
Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys  
35 40 45

<210> 33  
<211> 43  
<212> PRT  
<213> Vicia faba

<400> 33  
Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp Trp Asp  
1 5 10 15  
Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala Ser Arg  
20 25 30  
Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp  
35 40

<210> 34  
<211> 9  
<212> PRT  
<213> Vicia faba

<400> 34  
Leu Pro Asp Gly Ser Ile Leu Arg Cys  
1 5

<210> 35  
<211> 24  
<212> PRT  
<213> Vicia faba

<400> 35  
Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp Pro Leu His Asn Gly  
1 5 10 15  
Lys Thr Met Leu Lys Ile Trp Asn  
20

<210> 36  
<211> 13  
<212> PRT  
<213> Vicia faba

<400> 36  
Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp  
1 5 10

<210> 37  
<211> 9  
<212> PRT  
<213> Vicia faba

<400> 37  
Phe Ala Pro Ile Gly Leu Val Asn Met  
1 5

<210> 38  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (1)..(32)  
<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 1-F (from list 4)

<400> 38  
ttnaangtnt ggtggacnac ncantgggtn gg

32

<210> 39  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (1)..(41)  
<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 2-F (from list 4)

<400> 39  
atnatngana anttnggntg gtgnacntgg gangcnttnt a

41

<210> 40  
<211> 41  
<212> DNA

<213> Artificial Sequence

<220>

<221> modified\_base

<222> (1)..(41)

<223> n = inosine

<220>

<223> Description of Artificial Sequence:synthetic  
primer 2-RV (from list 4)

<400> 40

tanaangnt cccangtnca ccancnaa n ttntcnatna t

41

<210> 41

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<221> modified\_base

<222> (1)..(44)

<223> n = inosine

<220>

<223> Description of Artificial Sequence:synthetic  
primer 3-F (from list 4)

<400> 41

ggnggntgnc cncnggntt ngtnatnatn gangangnt ggca

44

<210> 42

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<221> modified\_base

<222> (1)..(44)

<223> n = inosine

<220>

<223> Description of Artificial Sequence:synthetic  
primer 3-RV (from list 4)

<400> 42

tgccancnt cntcnatnat nacnaancn ggnggncanc cncc

44

<210> 43

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<221> modified\_base

<222> (1)..(32)

<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 4-F (from list 4)

<400> 43  
aanaancant tnaangnaa ngngnntnatn gc

32

<210> 44  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (1)..(32)  
<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 4-RV (from list 4)

<400> 44  
gcnatnacnc cnttnccntt naantgnttn tt

32

<210> 45  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (1)..(38)  
<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 5-F (from list 4)

<400> 45  
tggatgggna anttnatnca nccngantgg ganatggt

38

<210> 46  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (1)..(38)  
<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 5-RV (from list 4)

<400> 46  
aacatntccc antcnggntg natnaanttn cccatcca

38

<210> 47  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (1)..(27)  
<223> n = inosine

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 6-RV (from list 4)

<400> 47  
catnttnacn arnccnatng gngcnaa

27

<210> 48  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 8.2 (from list 5)

<400> 48  
aaracngcnc cnagyathat hgacaa

26

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 13.4 (from list 5)

<400> 49  
aarathtgga ayctnaacaa

20

<210> 50  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 7.4 (from list 5)

<400> 50  
aargcnagrg tngtngtncc naag

24

<210> 51  
<211> 21  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 13.3RV (from list 5)

<400> 51

yttrtttnagr ttccadattt t

21

<210> 52

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 10.3RV (from list 5)

<400> 52

yttrtctyter tanagraatt t

21

<210> 53

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer RES-2RV (from list 6)

<400> 53

ggctgagggtt cggttcattc ctgaatcatc

30

<210> 54

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer RS-7 (from list 6)

<400> 54

ccaaatggta catattggct ccaaggttgt

30

<210> 55

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer RS-8 (from list 6)

<400> 55

aagagtgtat ctgaattttc acgcgcggtg

30

<210> 56  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer RS-9 (from list 6)

<400> 56  
tggtgcaatg ggaaaactcc aatgagcacc 30

<210> 57  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer RS-10 (from list 6)

<400> 57  
atgaagtgtt ctgatagatt gaaagtttcg 30

<210> 58  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer RS-11 (from list 6)

<400> 58  
cagtctctgg agtttgatga taatgcaagt 30

<210> 59  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer RS-N (from list 7)

<400> 59  
cgcggatcca ccatggcacc accaagcata accaaaactg c 41

<210> 60  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer RS-C (from list 7)

<220>  
 <221> modified\_base  
 <222> (1)..(37)  
 <223> n = inosine  
  
 <400> 60  
 tgctctagat tatcaaaata aaaactggac caaagac

37

<210> 61  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 1-F (from list 8)

<220>  
 <221> modified\_base  
 <222> (1)..(35)  
 <223> n= inosine

<400> 61  
 cgattnaang tntggtggac nacncantgg gtngg

35

<210> 62  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 2-RV (from list 8)

<220>  
 <221> modified\_base  
 <222> (1)..(45)  
 <223> n = inosine

<400> 62  
 ggcctanaan gntcccaang tncaccancc naantntn atnat

45

<210> 63  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 primer 5-F (from list 8)

<220>  
 <221> modified\_base  
 <222> (1)..(41)  
 <223> n = inosine

<400> 63



cgatggatgg gnaanttnat ncancngan tggganatgt t

41

<210> 64

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 6-RV (from list 8)

<220>

<221> modified\_base

<222> (1)..(32)

<223> n = inosine

<400> 64

ggccacatnt tnacnarncc natnggngcn aa

32

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer SN-1 (from list 9)

<400> 65

cacgaactgg ggcacgagac acagatgatg

30

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer SC-3RV (from list 9)

<400> 66

aagcaagtca cggagtgtga atagtcagag

30

<210> 67

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer SC-5 (from list 9)

<400> 67

acacgagact gtttgtttga agacccttg

30

<210> 68

<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer SC-6 (from list 9)

<400> 68  
tggaatctca acaaataatac aggtg

25

<210> 69  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer SN-3RV (from list 9)

<400> 69  
gggtcatggc caacgtggac gtataagcac

30

<210> 70  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer SN-4RV (from list 9)

<400> 70  
gatgatcact ggcgcggttt tctcctcgag

30

<210> 71  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 1-F (from list 10)

<220>  
<221> modified\_base  
<222> (1)..(35)  
<223> n = inosine

<400> 71  
cgattnaang tntggtggac nacncantgg gtngg

35

<210> 72  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 4-RV (from list 10)

<220>  
<221> modified\_base  
<222> (1)..(37)  
<223> n = inosine

<400> 72  
ggccagcnat nacnccnttn ccnttnaant gnttntt

37

<210> 73  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 2-F (from list 10)

<220>  
<221> modified\_base  
<222> (1)..(44)  
<223> n = inosine

<400> 73  
cgaatnatng anaantnngg ntggtnacn tgggangent tnta

44

<210> 74  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 6-RV (from list 10)

<220>  
<221> modified\_base  
<222> (1)..(32)  
<223> n = inosine

<400> 74  
ggccacatnt tnacnarncc natngngcn aa

32

<210> 75  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 5-F (from list 11)

<220>  
<221> modified\_base  
<222> (1)..(41)

<223> n= inosine

<400> 75

cgatggatgg gnaanttnat ncancngan tggganatgt t

41

<210> 76

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer 6-RV (from list 11)

<220>

<221> modified\_base

<222> (1)..(32)

<223> n = inosine

<400> 76

ggccacatnt tnacnarncc natngngcn aa

32

<210> 77

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer M10 (from list 12)

<400> 77

gacgtcgagt ggaagagcgg caagg

25

<210> 78

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer M-11 (from list 12)

<400> 78

cacctacgag ctcttcgctg ttgcc

25

<210> 79

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
primer BamSac-(+) (from list 13)

<400> 79

gatcgagctc gtgtcggatc cagct

25

<210> 80  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer BamSac-(-) (from list 13)

<400> 80  
ggatccgaca cgagctc

17

<210> 81  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer 35S (from list 14)

<400> 81  
ttccagtatg gacgattcaa ggcttgcttc

30

<210> 82  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer NOS (from list 14)

<400> 82  
atgtataatt gcgggactct aatca

25

<210> 83  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
primer RS-F (from list 14)

<400> 83  
aagagtgtat ctgaattttc acgcgcggtg

30

<210> 84  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic

primer RS-RV (from list 14)

<400> 84

accttcccat acaccttttg gatgaacctt caa

33

<210> 85

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: BamHI-NcoI  
linker (from Fig. 1)

<400> 85

ggatccacca tggcaccacc aagcataacc aaaactgc

38

<210> 86

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: XbaI-NotI-SacI  
linker (from Fig. 1)

<400> 86

tgataatcta gagcggccgc caccgcggtg gagctc

36